SEQUENCE LISTING

<110> UNIVERSITY OF SOUTHERN CALIFORNIA
Markland, Francis S.
Ritter, Matthew

<120> CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METASTASIS AND OTHER CONDITIONS

<130> 1279-338N3/09801388

<140> Not yet assigned
<141> 2003-11-12

<150> US09/591,552
<151> 2000-06-08

<150> US 08/141,321
<151> 1993-10-22

<150> US 08/540,423
<151> 1995-10-10

<150> US 08/632,691
<151> 1996-04-15

<150> US 08/745,603
<151> 1996-11-08

<150> US 09/163,047
<151> 1998-09-29

<150> US09/460,295
<151> 1999-12-10

<160> 15

<170> PatentIn version 3.1

<210> 1
<211> 2029
<212> DNA
<213> Agkistrodon contortrix

<400> 1
gaattcgggg tcaatagagg aagagctcaa gttggcttga aagcaggaag agattgcctg 60

tcttccagcc aaatccagcc gccaaaatga tccaggttct cttggtgact ctatgcttag 120

cagcttttcc ttatcaaggg agctctataa tcctggaatc tgggaatgtt aatgattatg 180

aagtactgta tccacaaaaa gtcactgcat tgcccaaagg agcagttcag ccaaagtatg 240

aagacaccat gcaatatgaa tttaaagtga atggagagcc agtggtcctt cacctggaaa 300

aaaataaagg actttttca aaagattaca gcgagactca ttattcctct gatggcagaa 360

aaattacaac aaaccctccg gttgaggatc actgctatta tcatggacgc atccagaatg 420

atgctgactc aactgcaagc atcagtgcat gcaacggttt gaaaggacat ttcaagcttc 480

aaggggagac gtaccttatt gaacccttga agctttccga cagtgaagcc catgcagtct 540

acaaatatga aaacgtagaa aaagaagatg aggcccccaa aatgtgtggg gtaacccaga 600

ctaattggga atcagatgag cccatcaaaa aggcctctca gttaaatctt actcctgaac 660

aacaaggatt cccccaaaga tacattgagc ttgttgtagt tgcagatcac agaatgttca 720

cgaaatacaa cggcaattta aatactatta gaatatgggt acatgaactt gtcaacacta 780

tgaatgtgtt ttacagacct ttgaatattc gtgtctcact gactgaccta gaagtttggt 840

cagaccaaga tttgatcaac gtgcagccag cagcggctga tactttggaa gcatttggag 900

actggagaga gacagtcttg ctgaatcgca taagtcatga taatgctcag ttactcacgg 960

ccattgagct tgatggagaa actataggat tggctaacag gggcaccatg tgcgacccga 1020

agctttctac aggaattgtt caggatcata gtgcaataaa tctttgggtt gcagttacaa 1080

tgccccatga gatgggtcat aatctgggta ttagtcacga tggaaatcag tgtcattgcg 1140

atgctaactc atgcattatg agtgaagaac taagagaaca actttccttt gagttcagcg 1200

attgtagtca gaatcaatat cagacatatc ttactgatca taacccacaa tgcatgctca 1260

atgaaccctt gagaacagat attgtttcaa ctccagtttc tggaaatgaa cttttggaga 1320

cgggagaaga aagtgacttt gacgctcctg caaatccgtg ctgcgatgct gcaacatgta 1380

aactgacaac agggtcacag tgtgcagatg gactgtgttg tgaccagtgc aaatttatga 1440

aagaaggaac agtatgccgg agagcaaggg gtgatgacct ggatgattac tgcaatggca 1500

tatctgctgg ctgtcccaga aatcccttcc atgcctaacc aacaatggag atggaatggt 1560

ctgcagcaac aggcagtgtg ttgatctgaa tacagcctaa taatcaacct ctggcttctc 1620

tcagatttga tcatggagat ccttcttcca gaaggtttca cttccctcaa atccaaagag 1680

acccatctgc ctgcatccta ctagtaaatc acccttagct tccagatggt atccaaattc 1740

tgtaatattt cttctccata tttaatctat ttacctttg ctgtaacaaa acctttttcc 1800

tgtcacaaag ctccatgggc atgtacagct tatctgctgt caagaaaaaa aatggccatt 1860

ttaccgtttg ccagttacaa agcacattta atgcaacaag ttcttccttt tgagctgatg 1920

tattcaaagt caatgcttcc tctcccaaaa tttcatgctg gcttcccaag atgtagctgc 1980

ttccgtcaat aaacaaacta ttctcattca aaaaaaaaaa cccgaattc 2029

<210> 2
<211> 483
<212> PRT
<213> Agkistrodon contortrix

<400> 2

```
Met Ile Gln Val Leu Leu Val Thr Leu Cys Leu Ala Ala Phe Pro Tyr
1               5                  10                  15

Gln Gly Ser Ser Ile Ile Leu Glu Ser Gly Asn Val Asn Asp Tyr Glu
            20                  25                  30

Val Leu Tyr Pro Gln Lys Val Thr Ala Leu Pro Lys Gly Ala Val Gln
        35                  40                  45

Pro Lys Tyr Glu Asp Thr Met Gln Tyr Glu Phe Lys Val Asn Gly Glu
    50                  55                  60

Pro Val Val Leu His Leu Glu Lys Asn Lys Gly Leu Phe Ser Lys Asp
65                  70                  75                  80

Tyr Ser Glu Thr His Tyr Ser Ser Asp Gly Arg Lys Ile Thr Thr Asn
                85                  90                  95

Pro Pro Val Glu Asp His Cys Tyr Tyr His Gly Arg Ile Gln Asn Asp
            100                 105                 110

Ala Asp Ser Thr Ala Ser Ile Ser Ala Cys Asn Gly Leu Lys Gly His
        115                 120                 125

Phe Lys Leu Gln Gly Glu Thr Tyr Leu Ile Glu Pro Leu Lys Leu Ser
    130                 135                 140

Asp Ser Glu Ala His Ala Val Tyr Lys Tyr Glu Asn Val Glu Lys Glu
145                 150                 155                 160

Asp Glu Ala Pro Lys Met Cys Gly Val Thr Gln Thr Asn Trp Glu Ser
                165                 170                 175

Asp Glu Pro Ile Lys Lys Ala Ser Gln Leu Asn Leu Thr Pro Glu Gln
            180                 185                 190

Gln Gly Phe Pro Gln Arg Tyr Ile Glu Leu Val Val Val Ala Asp His
        195                 200                 205
```

```
Arg Met Phe Thr Lys Tyr Asn Gly Asn Leu Asn Thr Ile Arg Ile Trp
    210                 215                 220

Val His Glu Leu Val Asn Thr Met Asn Val Phe Tyr Arg Pro Leu Asn
225                 230                 235                 240

Ile Arg Val Ser Leu Thr Asp Leu Glu Val Trp Ser Asp Gln Asp Leu
                245                 250                 255

Ile Asn Val Gln Pro Ala Ala Ala Asp Thr Leu Glu Ala Phe Gly Asp
            260                 265                 270

Trp Arg Glu Thr Val Leu Leu Asn Arg Ile Ser His Asp Asn Ala Gln
        275                 280                 285

Leu Leu Thr Ala Ile Glu Leu Asp Gly Glu Thr Ile Gly Leu Ala Asn
    290                 295                 300

Arg Gly Thr Met Cys Asp Pro Lys Leu Ser Thr Gly Ile Val Gln Asp
305                 310                 315                 320

His Ser Ala Ile Asn Leu Trp Val Ala Val Thr Met Ala His Glu Met
                325                 330                 335

Gly His Asn Leu Gly Ile Ser His Asp Gly Asn Gln Cys His Cys Asp
            340                 345                 350

Ala Asn Ser Cys Ile Met Ser Glu Glu Leu Arg Glu Gln Leu Ser Phe
        355                 360                 365

Glu Phe Ser Asp Cys Ser Gln Asn Gln Tyr Gln Thr Tyr Leu Thr Asp
    370                 375                 380

His Asn Pro Gln Cys Met Leu Asn Glu Pro Leu Arg Thr Asp Ile Val
385                 390                 395                 400

Ser Thr Pro Val Ser Gly Asn Glu Leu Leu Glu Thr Gly Glu Glu Ser
                405                 410                 415

Asp Phe Asp Ala Pro Ala Asn Pro Cys Cys Asp Ala Ala Thr Cys Lys
            420                 425                 430
```

Leu Thr Thr Gly Ser Gln Cys Ala Asp Gly Leu Cys Cys Asp Gln Cys
435 440 445

Lys Phe Met Lys Glu Gly Thr Val Cys Arg Arg Ala Arg Gly Asp Asp
450 455 460

Leu Asp Asp Tyr Cys Asn Gly Ile Ser Ala Gly Cys Pro Arg Asn Pro
465 470 475 480

Phe His Ala

<210> 3
<211> 21
<212> DNA
<213> Trimeresurus gramineus

<400> 3
gtttacaggt tgcagcatcg c 21

<210> 4
<211> 21
<212> DNA
<213> Trimeresurus gramineus

<400> 4
gcgatgctgc aacctgtaaa c 21

<210> 5
<211> 21
<212> DNA
<213> Bacteriophage lambda

<400> 5
gcgatgctgc aacctgtaaa c 21

<210> 6
<211> 24
<212> DNA
<213> Bacteriophaeg Lambda gt10

<400> 6
cttatgagta tttcttccag ggta 24

<210> 7
<211> 71
<212> PRT
<213> Agkistrodon piscivorus

<400> 7

```
Glu Ala Gly Glu Glu Cys Asp Cys Gly Ser Pro Glu Asn Pro Cys Cys
1               5                   10                  15

Asp Ala Ala Thr Cys Lys Leu Arg Pro Gly Ala Gln Cys Ala Glu Gly
            20                  25                  30

Leu Cys Cys Asp Gln Cys Lys Phe Met Lys Glu Gly Thr Val Cys Arg
        35                  40                  45

Ala Arg Gly Asp Asp Val Asn Asp Tyr Cys Asn Gly Ile Ser Ala Gly
    50                  55                  60

Cys Pro Arg Asn Pro Phe His
65                  70
```

<210> 8
<211> 552
<212> PRT
<213> Trimeresurus gramineus

<400> 8

```
Glu Ala Gly Glu Asp Cys Asp Cys Gly Ser Pro Ala Asn Pro Cys Cys
1               5                   10                  15

Asp Ala Ala Thr Cys Lys Leu Ile Pro Gly Ala Gln Cys Gly Glu Gly
            20                  25                  30

Leu Cys Cys Asp Gln Cys Ser Phe Ile Glu Glu Gly Thr Val Cys Arg
        35                  40                  45

Ile Ala Arg Gly Asp Asp Leu Asp Asp Tyr Cys Asn Gly Arg Ser Ala
    50                  55                  60

Gly Cys Pro Arg Asn Pro Phe His Met Ile Gln Val Leu Leu Ile Thr
65                  70                  75                  80

Ile Cys Leu Ala Val Phe Pro Tyr Gln Gly Ser Ser Ile Ile Leu Glu
                85                  90                  95

Ser Gly Asn Leu Asn Asp Tyr Glu Val Val Tyr Pro Glu Lys Val Thr
            100                 105                 110
```

```
Ala Leu Pro Lys Gly Ala Val Gln Gln Lys Tyr Glu Asp Ala Met Gln
        115                 120                 125

Tyr Glu Phe Lys Val Asn Gly Glu Pro Val Val Leu His Leu Glu Lys
    130                 135                 140

Asn Lys Gly Leu Phe Ser Glu Asp Tyr Ser Glu Ile His Tyr Ser Pro
145                 150                 155                 160

Asp Gly Arg Glu Ile Thr Ala Tyr Pro Ser Val Glu Asp His Cys Tyr
                165                 170                 175

Tyr His Gly Arg Ile Glu Asn Asp Ala Asp Ser Thr Ala Ser Ile Ser
            180                 185                 190

Ala Cys Asp Gly Leu Lys Gly His Phe Lys Leu Gln Gly Glu Met Tyr
        195                 200                 205

Leu Ile Glu Pro Leu Glu Leu Ser Asp Ser Glu Ala His Ala Val Phe
    210                 215                 220

Lys Tyr Glu Asn Val Glu Lys Glu Asp Glu Pro Pro Lys Met Cys Gly
225                 230                 235                 240

Val Thr Gln Asn Trp Glu Ser Tyr Glu Ser Thr Lys Lys Ala Ser Gln
                245                 250                 255

Leu Asn Val Thr Pro Glu Gln Gln Arg Phe Pro Gln Arg Tyr Ile Lys
            260                 265                 270

Leu Gly Ile Phe Val Asp His Gly Met Tyr Thr Lys Tyr Ser Gly Asn
        275                 280                 285

Ser Glu Arg Ile Thr Lys Arg Val His Gln Met Ile Asn Asn Ile Asn
    290                 295                 300

Met Met Cys Arg Ala Leu Asn Ile Val Thr Thr Leu Ser Val Leu Glu
305                 310                 315                 320

Ile Trp Ser Glu Lys Asp Leu Ile Thr Val Gln Ala Ser Ala Pro Thr
                325                 330                 335
```

```
Thr Leu Thr Leu Phe Gly Ala Trp Arg Glu Thr Val Leu Leu Asn Arg
            340                 345                 350

Thr Ser His Asp His Ala Gln Leu Leu Thr Ala Thr Ile Phe Asn Gly
        355                 360                 365

Asn Val Ile Gly Arg Ala Pro Val Gly Gly Met Cys Asp Pro Lys Arg
    370                 375                 380

Ser Val Ala Ile Val Arg Asp His Asn Ala Ile Val Phe Val Val Ala
385                 390                 395                 400

Val Thr Met Thr His Glu Met Gly His Asn Leu Gly Met His His Asp
                405                 410                 415

Glu Asp Lys Cys Asn Cys Asn Thr Cys Ile Met Ser Lys Val Leu Ser
            420                 425                 430

Arg Gln Pro Ser Lys Tyr Phe Ser Glu Cys Ser Lys Asp Tyr Tyr Gln
        435                 440                 445

Thr Phe Leu Thr Asn His Asn Pro Gln Cys Ile Leu Asn Ala Pro Leu
    450                 455                 460

Arg Thr Asp Thr Val Ser Thr Pro Val Ser Gly Asn Glu Leu Leu Glu
465                 470                 475                 480

Ala Gly Glu Asp Cys Asp Cys Gly Ser Pro Ala Asn Pro Cys Cys Asp
                485                 490                 495

Ala Ala Thr Cys Lys Leu Ile Pro Gly Ala Gln Cys Gly Glu Gly Leu
            500                 505                 510

Cys Cys Asp Gln Cys Ser Phe Ile Glu Glu Gly Thr Val Cys Arg Ile
        515                 520                 525

Ala Arg Gly Asp Asp Leu Asp Asp Tyr Cys Asn Gly Arg Ser Ala Gly
    530                 535                 540

Cys Pro Arg Asn Pro Phe His Ala
545                 550
```

<210> 9

<211> 73
<212> PRT
<213> Trimeresurus albolabris

<400> 9

Glu Ala Gly Glu Asp Cys Asp Cys Gly Ser Pro Ala Asn Pro Cys Cys
1 5 10 15

Asp Ala Ala Thr Cys Lys Leu Leu Pro Gly Ala Gln Cys Gly Glu Gly
20 25 30

Leu Cys Cys Asp Gln Cys Ser Phe Met Lys Lys Gly Thr Ile Cys Arg
35 40 45

Arg Ala Arg Gly Asp Asp Leu Asp Asp Tyr Cys Asn Gly Ile Ser Ala
50 55 60

Gly Cys Pro Arg Asn Pro Leu His Ala
65 70

<210> 10
<211> 73
<212> PRT
<213> Trimeresurus elegans

<400> 10

Glu Ala Gly Glu Glu Cys Asp Cys Gly Ser Pro Glu Asn Pro Cys Cys
1 5 10 15

Asp Ala Ala Thr Cys Lys Leu Arg Pro Gly Ala Gln Cys Ala Asp Gly
20 25 30

Leu Cys Cys Asp Gln Cys Arg Phe Lys Lys Lys Arg Thr Ile Cys Arg
35 40 45

Arg Ala Arg Gly Asp Asn Pro Asp Asp Arg Cys Thr Gly Gln Ser Ala
50 55 60

Asp Cys Pro Arg Asn Gly Leu Tyr Ser
65 70

<210> 11
<211> 68
<212> PRT
<213> Calloselasma rhodostoma

<400> 11

```
Gly Lys Glu Cys Asp Cys Ser Ser Pro Glu Asn Pro Cys Cys Asp Ala
1               5                   10                  15

Ala Thr Cys Lys Leu Arg Pro Gly Ala Gln Cys Gly Glu Gly Leu Cys
            20                  25                  30

Cys Glu Gln Cys Lys Phe Asp Arg Ala Gly Lys Ile Cys Arg Ile Pro
        35                  40                  45

Arg Gly Asp Met Pro Asp Asp Arg Cys Thr Gly Gln Ser Ala Asp Cys
    50                  55                  60

Pro Arg Tyr His
65
```

<210> 12
<211> 606
<212> PRT
<213> Crotalus atrox

<400> 12

```
Met Ile Gln Val Leu Leu Val Thr Ile Cys Leu Ala Ala Phe Pro Tyr
1               5                   10                  15

Gln Gly Ser Ser Ile Ile Leu Glu Ser Gly Asn Val Asn Asp Tyr Glu
            20                  25                  30

Val Ile Tyr Pro Arg Lys Val Thr Ala Leu Pro Lys Gly Ala Val Gln
        35                  40                  45

Pro Lys Tyr Glu Asp Ala Met Gln Tyr Glu Leu Lys Val Asn Gly Glu
    50                  55                  60

Pro Val Val Leu His Leu Gly Lys Asn Lys Gly Leu Phe Ser Lys Asp
65                  70                  75                  80

Tyr Ser Glu Thr His Tyr Ser Pro Asp Gly Arg Glu Ile Thr Thr Tyr
                85                  90                  95

Pro Leu Val Glu Asp His Cys Tyr Tyr His Gly Ile Glu Asn Asp Ala
            100                 105                 110
```

```
Asp Ser Thr Ala Ser Ile Ser Ala Cys Asn Gly Leu Lys Gly His Phe
        115                 120                 125

Lys Leu Gln Gly Glu Met Tyr Leu Ile Glu Pro Leu Lys Leu Pro Asp
    130                 135                 140

Ser Glu Ala His Ala Val Tyr Lys Tyr Glu Asn Val Glu Lys Glu Asp
145                 150                 155                 160

Glu Ala Leu Lys Met Cys Gly Val Thr Gln Asn Trp Glu Ser Tyr Glu
                165                 170                 175

Pro Ile Lys Lys Ala Ser Gln Leu Val Val Thr Ala Glu His Gln Lys
            180                 185                 190

Tyr Asn Pro Phe Arg Phe Val Glu Leu Phe Leu Val Val Asp Lys Ala
        195                 200                 205

Met Val Thr Lys Asn Asn Gly Asp Leu Asp Lys Ile Lys Thr Arg Met
    210                 215                 220

Tyr Glu Ile Val Asn Thr Val Asn Glu Ile Tyr Arg Tyr Met Tyr Ile
225                 230                 235                 240

His Val Ala Leu Val Gly Leu Glu Ile Trp Ser Asn Glu Asp Lys Ile
                245                 250                 255

Thr Val Lys Pro Glu Ala Gly Tyr Thr Leu Asn Ala Phe Gly Glu Trp
            260                 265                 270

Arg Lys Thr Asp Leu Leu Thr Arg Lys Lys His Asp Asn Ala Gln Leu
        275                 280                 285

Leu Thr Ala Ile Asp Leu Asp Arg Val Ile Gly Leu Ala Tyr Val Gly
    290                 295                 300

Ser Met Cys His Pro Lys Arg Ser Thr Gly Ile Ile Gln Asp Tyr Ser
305                 310                 315                 320

Glu Ile Asn Leu Val Val Ala Val Ile Met Ala His Glu Met Gly His
                325                 330                 335
```

```
Asn Leu Gly Ile Asn His Asp Ser Gly Tyr Cys Ser Cys Gly Asp Tyr
            340                 345                 350

Ala Cys Ile Met Arg Pro Glu Ile Ser Pro Glu Pro Ser Thr Phe Phe
        355                 360                 365

Ser Asn Cys Ser Tyr Phe Glu Cys Trp Asp Phe Ile Met Asn His Asn
    370                 375                 380

Pro Glu Cys Ile Leu Asn Glu Pro Leu Gly Thr Asp Ile Ile Ser Pro
385                 390                 395                 400

Pro Val Cys Gly Asn Glu Leu Leu Glu Val Gly Glu Glu Cys Asp Cys
                405                 410                 415

Gly Thr Pro Glu Asn Cys Gln Asn Glu Cys Cys Asp Ala Ala Thr Cys
            420                 425                 430

Lys Leu Lys Ser Gly Ser Gln Cys Gly His Gly Asp Cys Cys Glu Gln
        435                 440                 445

Cys Lys Phe Ser Lys Ser Gly Thr Glu Cys Arg Ala Ser Met Glu Cys
    450                 455                 460

Asp Pro Ala Glu His Cys Thr Gly Gln Ser Ser Glu Cys Pro Ala Asp
465                 470                 475                 480

Val Phe His Lys Asn Gly Gln Pro Cys Leu Asp Asn Tyr Gly Tyr Cys
                485                 490                 495

Tyr Asn Gly Asn Cys Pro Ile Met Tyr His Gln Cys Tyr Asp Leu Phe
            500                 505                 510

Gly Ala Asp Val Tyr Glu Ala Glu Asp Ser Cys Phe Glu Arg Asn Gln
        515                 520                 525

Lys Gly Asn Tyr Tyr Gly Tyr Cys Arg Lys Glu Asn Gly Asn Lys Ile
    530                 535                 540

Pro Cys Ala Pro Glu Asp Val Lys Cys Gly Arg Leu Tyr Cys Lys Asp
545                 550                 555                 560

Asn Ser Pro Gly Asn Asn Pro Cys Lys Met Glu Tyr Ser Asn Glu Asp
```

565 570 575

Glu His Lys Gly Met Val Leu Pro Gly Thr Lys Cys Ala Asp Gly Lys
580 585 590

Val Cys Ser Asn Gly His Cys Val Asp Val Ala Thr Ala Tyr
595 600 605

<210> 13
<211> 571
<212> PRT
<213> Bothrops jararaca

<400> 13

Ala Thr Arg Pro Lys Gly Ala Val Gln Pro Lys Tyr Glu Asp Ala Met
1 5 10 15

Gln Tyr Glu Phe Lys Val Asn Gly Glu Pro Val Val Leu His Leu Glu
20 25 30

Lys Asn Lys Gly Leu Phe Ser Lys Asp Tyr Ser Glu Ile His Tyr Ser
35 40 45

Pro Asp Gly Arg Glu Ile Thr Thr Tyr Pro Pro Val Glu Asp His Cys
50 55 60

Tyr Tyr His Gly Arg Ile Glu Asn Asp Ala Asp Ser Thr Ala Ser Ile
65 70 75 80

Ser Ala Cys Asn Gly Leu Lys Gly Tyr Phe Lys Leu Gln Arg Glu Thr
85 90 95

Tyr Phe Ile Glu Pro Leu Lys Leu Pro Asp Ser Glu Ala His Ala Val
100 105 110

Phe Lys Tyr Glu Asn Val Glu Lys Glu Asp Glu Ala Pro Lys Met Cys
115 120 125

Gly Val Thr Gln Asn Trp Lys Ser Tyr Glu Pro Ile Lys Lys Ala Ser
130 135 140

Gln Leu Ala Phe Thr Ala Glu Gln Gln Arg Tyr Asp Pro Tyr Lys Tyr
145 150 155 160

```
Ile Glu Phe Phe Val Val Val Asp Gln Gly Thr Val Thr Lys Asn Asn
                165                 170                 175

Gly Asp Leu Asp Lys Ile Lys Ala Arg Met Tyr Glu Leu Ala Asn Ile
            180                 185                 190

Val Asn Glu Ile Phe Arg Tyr Leu Tyr Met His Val Ala Leu Val Gly
        195                 200                 205

Leu Glu Ile Trp Ser Asn Gly Asp Lys Ile Thr Val Lys Pro Asp Val
    210                 215                 220

Asp Tyr Thr Leu Asn Ser Phe Ala Glu Trp Arg Lys Thr Asp Leu Leu
225                 230                 235                 240

Thr Arg Lys Lys His Asp Asn Ala Gln Leu Leu Thr Ala Ile Asp Phe
                245                 250                 255

Asn Gly Pro Thr Ile Phe Tyr Ala Tyr Ile Gly Ser Met Cys His Pro
            260                 265                 270

Lys Arg Ser Val Gly Ile Val Gln Asp Tyr Ser Pro Ile Asn Leu Val
        275                 280                 285

Val Ala Val Ile Met Ala His Glu Met Gly His Asn Leu Gly Ile His
    290                 295                 300

His Asp Thr Gly Ser Cys Ser Cys Gly Asp Tyr Pro Cys Ile Met Gly
305                 310                 315                 320

Pro Thr Ile Ser Asn Glu Pro Ser Lys Phe Phe Ser Asn Cys Ser Tyr
                325                 330                 335

Ile Gln Cys Trp Asp Phe Ile Met Asn His Asn Pro Glu Cys Ile Ile
            340                 345                 350

Asn Glu Pro Leu Gly Thr Asp Ile Ile Ser Pro Pro Val Cys Gly Asn
        355                 360                 365

Glu Leu Leu Glu Val Gly Glu Glu Cys Asp Cys Gly Thr Pro Glu Asn
    370                 375                 380
```

```
Cys Gln Asn Glu Cys Cys Asp Ala Ala Thr Cys Lys Leu Lys Ser Gly
385                 390                 395                 400

Ser Gln Cys Gly His Gly Asp Cys Cys Glu Gln Cys Lys Phe Ser Lys
                405                 410                 415

Ser Gly Thr Glu Cys Arg Ala Ser Met Ser Glu Cys Asp Pro Ala Glu
            420                 425                 430

His Cys Thr Gly Gln Ser Ser Glu Cys Pro Ala Asp Val Phe His Lys
        435                 440                 445

Asn Gly Gln Pro Cys Leu Asp Asn Tyr Gly Tyr Cys Tyr Asn Gly Asn
    450                 455                 460

Cys Pro Ile Met Tyr His Gln Cys Tyr Ala Leu Phe Gly Ala Asp Val
465                 470                 475                 480

Tyr Glu Ala Glu Asp Ser Cys Phe Lys Asp Asn Gln Lys Gly Asn Tyr
                485                 490                 495

Tyr Gly Tyr Cys Arg Lys Glu Asn Gly Lys Lys Ile Pro Cys Ala Pro
            500                 505                 510

Glu Asp Val Lys Cys Gly Arg Leu Tyr Cys Lys Asp Asn Ser Pro Gly
        515                 520                 525

Gln Asn Asn Pro Cys Lys Met Phe Tyr Ser Asn Asp Asp Glu His Lys
    530                 535                 540

Gly Met Val Leu Pro Gly Thr Lys Cys Ala Asp Gly Lys Val Cys Ser
545                 550                 555                 560

Asn Gly His Cys Val Asp Val Ala Thr Ala Tyr
                565                 570
```

<210> 14
<211> 478
<212> PRT
<213> Crotalus atrox

<400> 14

```
Met Ile Gln Val Leu Leu Val Thr Ile Cys Leu Ala Ala Phe Pro Tyr
1               5                   10                  15
```

```
Gln Gly Ser Ser Ile Ile Leu Glu Ser Gly Asn Val Asn Asp Tyr Glu
            20                  25                  30

Val Ile Tyr Pro Arg Lys Val Thr Ala Leu Pro Lys Gly Ala Val Gln
        35                  40                  45

Pro Lys Tyr Glu Asp Thr Met Gln Tyr Glu Leu Lys Val Asn Gly Glu
    50                  55                  60

Pro Val Val Leu His Leu Glu Lys Asn Lys Gly Leu Phe Ser Lys Asp
65                  70                  75                  80

Tyr Ser Glu Thr His Tyr Ser Phe Asp Gly Arg Lys Ile Thr Thr Asn
                85                  90                  95

Pro Ser Val Glu Asp His Cys Tyr Tyr His Gly Arg Ile Glu Asn Asp
            100                 105                 110

Ala Asp Ser Thr Ala Ser Ile Ser Ala Cys Asn Gly Leu Lys Gly His
        115                 120                 125

Phe Lys Leu Gln Gly Glu Met Tyr Leu Ile Glu Pro Leu Lys Leu Ser
    130                 135                 140

Asp Ser Glu Ala His Ala Val Phe Lys Leu Lys Asn Val Glu Lys Glu
145                 150                 155                 160

Asp Glu Ala Pro Lys Met Cys Gly Val Thr Gln Asn Trp Glu Ser Tyr
                165                 170                 175

Glu Pro Ile Lys Lys Ala Ser Asp Leu Asn Leu Asn Pro Glu His Gln
            180                 185                 190

Arg Tyr Val Glu Leu Phe Ile Val Val Asp His Gly Met Tyr Thr Lys
        195                 200                 205

Tyr Asn Gly Asp Ser Asp Lys Ile Arg Gln Arg Val His Gln Met Val
    210                 215                 220

Asn Ile Met Lys Glu Ser Tyr Thr Tyr Met Tyr Ile Asp Ile Leu Leu
225                 230                 235                 240
```

```
Ala Gly Ile Glu Ile Trp Ser Asn Gly Asp Leu Ile Asn Val Gln Pro
                245                 250                 255

Ala Ser Pro Asn Thr Leu Asn Ser Phe Gly Glu Trp Arg Glu Thr Asp
            260                 265                 270

Leu Leu Lys Arg Lys Ser His Asp Asn Ala Gln Leu Leu Thr Ser Ile
        275                 280                 285

Ala Phe Asp Glu Gln Ile Ile Gly Arg Ala Tyr Ile Gly Gly Ile Cys
    290                 295                 300

Asp Pro Lys Arg Ser Thr Gly Val Val Gln Asp His Ser Glu Ile Asn
305                 310                 315                 320

Leu Arg Val Ala Val Thr Met Thr His Glu Leu Gly His Asn Leu Gly
                325                 330                 335

Ile His His Asp Thr Asp Ser Cys Ser Cys Gly Gly Tyr Ser Cys Ile
            340                 345                 350

Met Ser Pro Val Ile Ser Asp Glu Pro Ser Lys Tyr Phe Ser Asp Cys
        355                 360                 365

Ser Tyr Ile Gln Cys Trp Glu Phe Ile Met Asn Gln Lys Pro Gln Cys
    370                 375                 380

Ile Leu Lys Lys Pro Leu Arg Thr Asp Thr Val Ser Thr Pro Val Ser
385                 390                 395                 400

Gly Asn Glu Leu Leu Glu Ala Gly Ile Glu Cys Asp Gly Gly Ser Leu
                405                 410                 415

Glu Asn Pro Cys Cys Tyr Ala Thr Thr Cys Lys Met Arg Pro Gly Ser
            420                 425                 430

Gln Cys Ala Glu Gly Leu Cys Cys Asp Gln Cys Arg Phe Met Lys Lys
        435                 440                 445

Gly Thr Val Cys Arg Val Ser Met Val Asp Arg Asn Asp Asp Thr Cys
    450                 455                 460
```

Thr Gly Gln Ser Ala Asp Cys Pro Arg Asn Gly Leu Tyr Gly
465 470 475

<210> 15
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> RGD PEPTIDE

<400> 15

Gly Arg Gly Asp Ser Pro
1 5

SEQUENCE LISTING

<110> Markland, Francis S.
Ritter, Matthew

<120> Contortrostatin (CN) and Methods for its Use In Preventing Metastasis and Other Conditions

<130> USC/09801388/Markland et al

<140>
<141>

<150> 09/460,295
<151> 1999-12-10

<150> 09/163,047
<151> 1998-09-29

<150> 08/745,603
<151> 1996-11-08

<150> 08/632,691
<151> 1996-04-15

<150> 08/540,423
<151> 1995-10-10

<150> 08/141,321
<151> 1993-10-22

<160> 6

<170> PatentIn Ver. 2.1

<210> 1
<211> 2029
<212> DNA
<213> Agkistrodon contortrix

<400> 1
gaattcgggg tcaatagagg aagagctcaa gttggcttga aagcaggaag agattgcctg 60
tcttccagcc aaatccagcc gccaaaatga tccaggttct cttggtgact ctatgcttag 120
cagcttttcc ttatcaaggg agctctataa tcctggaatc tgggaatgtt aatgattatg 180
aagtactgta tccacaaaaa gtcactgcat tgcccaaagg agcagttcag ccaaagtatg 240
aagacaccat gcaatatgaa tttaaagtga atggagagcc agtggtcctt cacctggaaa 300
aaaataaagg actttttca aaagattaca gcgagactca ttattcctct gatggcagaa 360
aaattacaac aaaccctccg gttgaggatc actgctatta tcatggacgc atccagaatg 420

atgctgactc aactgcaagc atcagtgcat gcaacggttt gaaaggacat ttcaagcttc 480
aaggggagac gtaccttatt gaacccttga agctttccga cagtgaagcc catgcagtct 540
acaaatatga aaacgtagaa aaagaagatg aggcccccaa aatgtgtggg gtaacccaga 600
ctaattggga atcagatgag cccatcaaaa aggcctctca gttaaatctt actcctgaac 660
aacaaggatt cccccaaaga tacattgagc ttgttgtagt tgcagatcac agaatgttca 720
cgaaatacaa cggcaattta aatactatta gaatatgggt acatgaactt gtcaacacta 780
tgaatgtgtt ttacagacct ttgaatattc gtgtctcact gactgaccta gaagtttggt 840
cagaccaaga tttgatcaac gtgcagccag cagcggctga tactttggaa gcatttggag 900
actggagaga gacagtcttg ctgaatcgca taagtcatga taatgctcag ttactcacgg 960
ccattgagct tgatggagaa actataggat tggctaacag gggcaccatg tgcgacccga 1020
agctttctac aggaattgtt caggatcata gtgcaataaa tctttgggtt gcagttacaa 1080
tgccccatga gatgggtcat aatctgggta ttagtcacga tggaaatcag tgtcattgcg 1140
atgctaactc atgcattatg agtgaagaac taagagaaca actttccttt gagttcagcg 1200
attgtagtca gaatcaatat cagacatatc ttactgatca taacccacaa tgcatgctca 1260
atgaaccctt gagaacagat attgtttcaa ctccagtttc tggaaatgaa cttttggaga 1320
cgggagaaga aagtgacttt gacgctcctg caaatccgtg ctgcgatgct gcaacatgta 1380
aactgacaac agggtcacag tgtgcagatg gactgtgttg tgaccagtgc aaatttatga 1440
aagaaggaac agtatgccgg agagcaaggg gtgatgacct ggatgattac tgcaatggca 1500
tatctgctgg ctgtcccaga aatcccttcc atgcctaacc aacaatggag atggaatggt 1560
ctgcagcaac aggcagtgtg ttgatctgaa tacagcctaa taatcaacct ctggcttctc 1620
tcagatttga tcatggagat ccttcttcca gaaggtttca cttccctcaa atccaaagag 1680
acccatctgc ctgcatccta ctagtaaatc acccttagct tccagatggt atccaaattc 1740
tgtaatattt cttctccata tttaatctat ttacctttg ctgtaacaaa acctttttcc 1800
tgtcacaaag ctccatgggc atgtacagct tatctgctgt caagaaaaaa aatggccatt 1860
ttaccgtttg ccagttacaa agcacattta atgcaacaag ttcttccttt tgagctgatg 1920
tattcaaagt caatgcttcc tctcccaaaa tttcatgctg gcttcccaag atgtagctgc 1980
ttccgtcaat aaacaaacta ttctcattca aaaaaaaaaa cccgaattc 2029

<210> 2
<211> 483
<212> PRT
<213> Agkistrodon contortrix

<400> 2
Met Ile Gln Val Leu Leu Val Thr Leu Cys Leu Ala Ala Phe Pro Tyr
1 5 10 15

Gln Gly Ser Ser Ile Ile Leu Glu Ser Gly Asn Val Asn Asp Tyr Glu
20 25 30

Val Leu Tyr Pro Gln Lys Val Thr Ala Leu Pro Lys Gly Ala Val Gln
35 40 45

Pro Lys Tyr Glu Asp Thr Met Gln Tyr Glu Phe Lys Val Asn Gly Glu
50 55 60

Pro Val Val Leu His Leu Glu Lys Asn Lys Gly Leu Phe Ser Lys Asp

65 70 75 80

Tyr Ser Glu Thr His Tyr Ser Ser Asp Gly Arg Lys Ile Thr Thr Asn
85 90 95

Pro Pro Val Glu Asp His Cys Tyr Tyr His Gly Arg Ile Gln Asn Asp
100 105 110

Ala Asp Ser Thr Ala Ser Ile Ser Ala Cys Asn Gly Leu Lys Gly His
115 120 125

Phe Lys Leu Gln Gly Glu Thr Tyr Leu Ile Glu Pro Leu Lys Leu Ser
130 135 140

Asp Ser Glu Ala His Ala Val Tyr Lys Tyr Glu Asn Val Glu Lys Glu
145 150 155 160

Asp Glu Ala Pro Lys Met Cys Gly Val Thr Gln Thr Asn Trp Glu Ser
165 170 175

Asp Glu Pro Ile Lys Lys Ala Ser Gln Leu Asn Leu Thr Pro Glu Gln
180 185 190

Gln Gly Phe Pro Gln Arg Tyr Ile Glu Leu Val Val Val Ala Asp His
195 200 205

Arg Met Phe Thr Lys Tyr Asn Gly Asn Leu Asn Thr Ile Arg Ile Trp
210 215 220

Val His Glu Leu Val Asn Thr Met Asn Val Phe Tyr Arg Pro Leu Asn
225 230 235 240

Ile Arg Val Ser Leu Thr Asp Leu Glu Val Trp Ser Asp Gln Asp Leu
245 250 255

Ile Asn Val Gln Pro Ala Ala Ala Asp Thr Leu Glu Ala Phe Gly Asp
260 265 270

Trp Arg Glu Thr Val Leu Leu Asn Arg Ile Ser His Asp Asn Ala Gln
275 280 285

Leu Leu Thr Ala Ile Glu Leu Asp Gly Glu Thr Ile Gly Leu Ala Asn
290 295 300

Arg Gly Thr Met Cys Asp Pro Lys Leu Ser Thr Gly Ile Val Gln Asp
305 310 315 320

His Ser Ala Ile Asn Leu Trp Val Ala Val Thr Met Ala His Glu Met

325 330 335

Gly His Asn Leu Gly Ile Ser His Asp Gly Asn Gln Cys His Cys Asp
340 345 350

Ala Asn Ser Cys Ile Met Ser Glu Glu Leu Arg Glu Gln Leu Ser Phe
355 360 365

Glu Phe Ser Asp Cys Ser Gln Asn Gln Tyr Gln Thr Tyr Leu Thr Asp
370 375 380

His Asn Pro Gln Cys Met Leu Asn Glu Pro Leu Arg Thr Asp Ile Val
385 390 395 400

Ser Thr Pro Val Ser Gly Asn Glu Leu Leu Glu Thr Gly Glu Glu Ser
405 410 415

Asp Phe Asp Ala Pro Ala Asn Pro Cys Cys Asp Ala Ala Thr Cys Lys
420 425 430

Leu Thr Thr Gly Ser Gln Cys Ala Asp Gly Leu Cys Cys Asp Gln Cys
435 440 445

Lys Phe Met Lys Glu Gly Thr Val Cys Arg Arg Ala Arg Gly Asp Asp
450 455 460

Leu Asp Asp Tyr Cys Asn Gly Ile Ser Ala Gly Cys Pro Arg Asn Pro
465 470 475 480

Phe His Ala

<210> 3
<211> 21
<212> DNA
<213> Trimeresurus gramineus

<400> 3
gtttacaggt tgcagcatcg c 21

<210> 4
<211> 21
<212> DNA
<213> Trimeresurus gramineus

<400> 4

gcgatgctgc aacctgtaaa c 21

<210> 5
<211> 21
<212> DNA
<213> Bacteriophage Lambda gt10

<400> 5
gcgatgctgc aacctgtaaa c 21

<210> 6
<211> 24
<212> DNA
<213> Bacteriophage Lambda gt10

<400> 6
cttatgagta tttcttccag ggta 24